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RAW SEQUENCE LISTING
PATENT APPLICATION: -US/10/042,431

DATE: 01/27/2002
TIME: 15:34:20

Input Set : A:\101476ul.app
Output Set: N:\CRF3\01272002\J042431.raw

ENTERED

3 <110> APPLICANT: MCCARTHY, Sean A
4 BARNES, Thomas M
5 FRASER, Christopher C
6 SHARP, John D
8 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
9 PREVENTIVE, THERAPEUTIC, AND OTHER USES
11 <130> FILE REFERENCE: 10147-6U2
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/042,431
14 <141> CURRENT FILING DATE: 2001-10-25
16 <150> PRIOR APPLICATION NUMBER: US 09/333,159
17 <151> PRIOR FILING DATE: 1999-06-14
19 <150> PRIOR APPLICATION NUMBER: US 09/578,063
20 <151> PRIOR FILING DATE: 2000-05-24
22 <160> NUMBER OF SEQ ID NOS: 79
24 <170> SOFTWARE: PatentIn Ver. 2.1
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27 <211> LENGTH: 1656
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 cccggaccgg agtgtttcac agccaatggt gggattata gggaaacaca gaactggaca 180
35 gcactacaag gcgggaagcc atgtctgtt tggAACGAGA ctttcagca tccataacaac 240
36 actctgaaat accccaacgg ggaggggggc ctgggtgagc acaactattg cagaatcca 300
37 gatggagacg tgagccccctg gtgttatgtg gcagagcagc aggatgggtg ctactggaa 360
38 tacttgaga tacctgtttt ccagatgcct ggaaaccttg gctgtacaa ggatcatgaa 420
39 aacccacctc ctctaactgg caccagtaaa acgtccaaca aactcaccat acaaacttgc 480
40 atcagttttt gtcggagtca gaggttcaag ttgtctggg tggagtcaagg ctatgttgc 540
41 ttctgtggaa acaatctga ttactggaa tacggggagg cagccagtac cgaatgcaac 600
42 agcgtctgtc tggggatca caccacccc tgggtggcg atggcaggat catccttgc 660
43 gatactctcg tgggcgcctg cgggtggaaac tactcagcca tgtctctgt ggtctattcc 720
44 cctgacttcc ccgacaccta tgccacgggg agggtctgt actggaccat cggggttcgg 780
45 ggggcctccc acatccactt cagctcccc ctatggaca tcaggactc ggcggacatg 840
46 gtggagcttc tggatggata caccacccgt gtcctagccc gttccacgg gaggagccgc 900
47 ccacctctgt cttcaacgt ctctctggac ttctgtatct tgtatttctt ctctgtatcgc 960
48 atcaatcagg cccaggatt tgctgttttta taccagccg tcaaggaaga actgcccacag 1020
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50 gtcagcgctg cccggcttc caaagtccctc tatgtcatca ccaccagccc cagccaccca 1140
51 cctcagactg tcccaggtag caattctgg ggcgcaccca tggggctgg aagccacaga 1200
52 gttgaaggat ggacagtcta tggctggca actctccatca tcctcacagt cacagccatt 1260
53 gtagcaaaga tacttctgca cgtcacattc aaatcccattc gtgttctgc ttcagggac 1320
54 ctttagggatt gtcatcaacc agggacttcg gggaaatct ggagcatttt ttacaagct 1380

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55 tccacttcaa tttccatctt taagaagaaa ctcagggtc agagtcaaca agatgaccgc 1440
 56 aatccccctt tgagtgacta aaaacccac tgtgcctagg acttgagggtc cctcttttag 1500
 57 ctcagggtg ccgtggtaa cctctctgt gttcttctc tgacagactc ttccctcctc 1560
 58 tccctctgcc tcggcctctt cggggaaacc ctccctctac agactaggaa gaggcacctg 1620
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 69 gattataggg gaacacagaa ctggacagca ctacaaggcg ggaagccatg tctgttttg 180
 70 aacgagactt tccagcatcc atacaacact ctgaaatacc ccaacggggaa gggggggcctg 240
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 73 gggcggcagg atgggtgtcta ctggaaagtac tggatgtac ctgcttgcca gatgcctgga 420
 74 aaccctggct gctacaagga tcatggaaac ccaccccttc taactggcac cgtaaaaacg 480
 75 tccaacaaac tcaccataca aacttgcata agtggatgtc ggagtcagag gttcaagttt 540
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 78 ggtggcgatg gcaggatcat cctttgtat actctgtgg gggcctggcgg tggaaactac 720
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 85 gtatcacgg agcaggccaa cctcgtgtc agcgtgtccc gtcctccaa agtcccttat 1140
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 87 ccacccatgg gggctggaaag ccacagaggta gaaggatggc cgtctatgg tctggcaact 1260
 88 tccctcatcc tcacagtaccc accattgtt gcaagatata ttctgcacgt cacatcaaa 1320
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 90 gaaatcttgg gcattttta caaccccttcc acttcaattt ccatctttaa gaagaaactc 1425
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 95 <211> LENGTH: 475
 96 <212> TYPE: PRT
 97 <213> ORGANISM: Homo sapiens
 98 <400> SEQUENCE: 3
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 100 1 5 10 15
 101 Thr Leu Ala Ala Arg Pro Ala Pro Ser Pro Gly Leu Gly Pro Gly Pro
 102 20 25 30
 103 Glu Cys Phe Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp
 104 35 40 45
 105 Thr Ala Leu Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe
 106 50 55 60
 107 Gln His Pro Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Leu
 108 65 70 75 80
 109 70 75 80
 110 75 80
 111 80
 112 85
 113 90

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115	Gly	Glu	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Val	Ser	Pro	Trp
																95
116					85											
118	Cys	Tyr	Val	Ala	Glu	His	Glu	Asp	Gly	Val	Tyr	Trp	Lys	Tyr	Cys	Glu
119						100				105						110
121	Ile	Pro	Ala	Cys	Gln	Met	Pro	Gly	Asn	Leu	Gly	Cys	Tyr	Lys	Asp	His
122							115			120						125
124	Gly	Asn	Pro	Pro	Pro	Leu	Thr	Gly	Thr	Ser	Lys	Thr	Ser	Asn	Lys	Leu
125							130			135						140
127	Thr	Ile	Gln	Thr	Cys	Ile	Ser	Phe	Cys	Arg	Ser	Gln	Arg	Phe	Lys	Phe
128							145			150			155			160
130	Ala	Gly	Met	Glu	Ser	Gly	Tyr	Ala	Cys	Phe	Cys	Gly	Asn	Asn	Pro	Asp
131							165			170						175
133	Tyr	Trp	Lys	Tyr	Gly	Glu	Ala	Ala	Ser	Thr	Glu	Cys	Asn	Ser	Val	Cys
134							180			185						190
136	Phe	Gly	Asp	His	Thr	Gln	Pro	Cys	Gly	Gly	Asp	Gly	Arg	Ile	Ile	Leu
137							195			200			205			
139	Phe	Asp	Thr	Leu	Val	Gly	Ala	Cys	Gly	Gly	Asn	Tyr	Ser	Ala	Met	Ser
140							210			215			220			
142	Ser	Val	Val	Tyr	Ser	Pro	Asp	Phe	Pro	Asp	Thr	Tyr	Ala	Thr	Gly	Arg
143							225			230			235			240
145	Val	Cys	Tyr	Trp	Thr	Ile	Arg	Val	Pro	Gly	Ala	Ser	His	Ile	His	Phe
146							245			250			255			
148	Ser	Phe	Pro	Leu	Phe	Asp	Ile	Arg	Asp	Ser	Ala	Asp	Met	Val	Glu	Leu
149							260			265			270			
151	Leu	Asp	Gly	Tyr	Thr	His	Arg	Val	Leu	Ala	Arg	Phe	His	Gly	Arg	Ser
152							275			280			285			
154	Arg	Pro	Pro	Leu	Ser	Phe	Asn	Val	Ser	Leu	Asp	Phe	Val	Ile	Leu	Tyr
155							290			295			300			
157	Phe	Phe	Ser	Asp	Arg	Ile	Asn	Gln	Ala	Gln	Gly	Phe	Ala	Val	Leu	Tyr
158							305			310			315			320
160	Gln	Ala	Val	Lys	Glu	Glu	Leu	Pro	Gln	Glu	Arg	Pro	Ala	Val	Asn	Gln
161							325			330			335			
163	Thr	Val	Ala	Glu	Val	Ile	Thr	Glu	Gln	Ala	Asn	Leu	Ser	Val	Ser	Ala
164							340			345			350			
166	Ala	Arg	Ser	Ser	Lys	Val	Leu	Tyr	Val	Ile	Thr	Ser	Pro	Ser	His	
167							355			360			365			
169	Pro	Pro	Gln	Thr	Val	Pro	Gly	Ser	Asn	Ser	Trp	Ala	Pro	Pro	Met	Gly
170							370			375			380			
172	Ala	Gly	Ser	His	Arg	Val	Glu	Gly	Trp	Thr	Val	Tyr	Gly	Leu	Ala	Thr
173							385			390			395			400
175	Leu	Leu	Ile	Leu	Thr	Val	Thr	Ala	Ile	Val	Ala	Lys	Ile	Leu	Leu	His
176							405			410			415			
178	Val	Thr	Phe	Lys	Ser	His	Arg	Val	Pro	Ala	Ser	Gly	Asp	Leu	Arg	Asp
179							420			425			430			
181	Cys	His	Gln	Pro	Gly	Thr	Ser	Gly	Glu	Ile	Trp	Ser	Ile	Phe	Tyr	Lys
182							435			440			445			
184	Pro	Ser	Thr	Ser	Ile	Ser	Ile	Phe	Lys	Lys	Lys	Leu	Lys	Gly	Gln	Ser
185							450			455			460			
187	Gln	Gln	Asp	Asp	Arg	Asn	Pro	Leu	Val	Ser	Asp					

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192 <211> LENGTH: 19		
193 <212> TYPE: PRT		
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198 1		
200 Thr Leu Ala		
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205 <211> LENGTH: 456		
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207 <213> ORGANISM: Homo sapiens		
209 <400> SEQUENCE: 5		
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211 1		
213 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu	20	25 30
214 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro	35	40 45
216 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His		
217 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Leu Gly Glu His	55	60
219 50		
220 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val	70	75 80
223 65		
225 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala	85	90 95
226 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro		
228 100		
229 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln	115	120 125
231 115		
232 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met	130	135 140
234 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys		
235 145		
238 150		
240 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp	165	170 175
241 His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp Thr		
243 180		
244 Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser Ser Val Val	185	190
246 195		
247 Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys Tyr	200	205
249 210		
250 Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe Ser Phe Pro	215	220 240
252 225		
253 Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu Leu Asp Gly	230	235 255
255 245		
256 Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser Arg Pro Pro	250	255 270
258 260		
259 Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr Phe Phe Ser	265	265
261		

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262	275	280	285
264 Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr Gln Ala Val			
265 290	295	300	
267 Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln Thr Val Ala			320
268 305	310	315	
270 Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala Ala Arg Ser			335
271	325	330	
273 Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His Pro Pro Gln			350
274	340	345	
276 Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly Ala Gly Ser			365
277	355	360	
279 His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr Leu Leu Ile			380
280	370	375	
282 Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His Val Thr Phe			400
283 385	390	395	
285 Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp Cys His Gln			415
286	405	410	
288 Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys Pro Ser Thr			430
289	420	425	
291 Ser Ile Ser Ile Phe Lys Lys Leu Lys Gly Gln Ser Gln Gln Asp			445
292	435	440	
294 Asp Arg Asn Pro Leu Val Ser Asp			455
295	450		
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307 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu			
308	20	25	30
310 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro			
311	35	40	45
313 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Leu Gly Glu His			
314	50	55	60
316 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val			
317 65	70	75	80
319 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala			
320	85	90	95
322 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro			
323	100	105	110
325 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln			
326	115	120	125
328 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met			
329	130	135	140
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332 145	150	155	
334 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp			

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number